



## SEQUENCE LISTING

<110> Syngenta  
Jepson, Ian  
Martinez, Alberto  
Greenland, Andrew James

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<151> 1996-05-24

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<151> 2000-05-03

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 Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu  
 485 490 495  
 Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr  
 500 505 510  
 Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr  
 515 520 525  
 Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu  
 530 535 540  
 Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu  
 545 550 555 560  
 Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu  
 565 570 575  
 Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr  
 580 585 590  
 Leu Arg Ile Thr Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu  
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 Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu  
 610 615 620  
 Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg  
 625 630 635 640  
 Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro  
 645 650 655  
 Pro Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu Asp Glu Arg  
 660 665 670  
 Leu Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr  
 675 680 685  
 Ala Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala  
 690 695 700  
 Ala Gln His Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu  
 705 710 715 720  
 Thr Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln  
 725 730 735  
 Leu Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln  
 740 745 750  
 Leu Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu  
 755 760 765  
 Pro Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu  
 770 775 780  
 Ser Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile  
 785 790 795 800



Leu Leu Gln Gln Leu Met Lys Cys Asp Pro Pro Pro His Pro Met Gln  
 245 250 255  
 Gln Leu Leu Pro Glu Lys Leu Leu Met Glu Asn Arg Ala Lys Gly Thr  
 260 265 270  
 Pro Gln Leu Thr Ala Asn Gln Val Ala Val Ile Tyr Lys Leu Ile Trp  
 275 280 285  
 Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Ile  
 290 295 300  
 Thr Thr Glu Leu Glu Glu Glu Glu Asp Gln Glu His Glu Ala Asn Phe  
 305 310 315 320  
 Arg Tyr Ile Thr Glu Val Thr Ile Leu Thr Val Gln Leu Ile Val Glu  
 325 330 335  
 Phe Ala Lys Gly Leu Pro Ala Phe Ile Lys Ile Pro Gln Glu Asp Gln  
 340 345 350  
 Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met  
 355 360 365  
 Ala Arg Arg Tyr Asp His Asp Ser Asp Ser Ile Leu Phe Ala Asn Asn  
 370 375 380  
 Thr Ala Tyr Thr Lys Gln Thr Tyr Gln Leu Ala Gly Met Glu Glu Thr  
 385 390 395 400  
 Ile Asp Asp Leu Leu His Phe Cys Arg Gln Met Tyr Ala Leu Ser Ile  
 405 410 415  
 Asp Asn Val Glu Thr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp  
 420 425 430  
 Arg Pro Gly Leu Glu Lys Ala Glu Met Val Asp Ile Ile Gln Ser Tyr  
 435 440 445  
 Tyr Thr Glu Thr Leu Lys Val Tyr Ile Val Arg Asp His Gly Gly Glu  
 450 455 460  
 Ser Arg Cys Ser Val Gln Phe Ala Lys Leu Leu Gly Ile Leu Thr Glu  
 465 470 475 480  
 Leu Arg Thr Met Gly Asn Leu Asn Ser Glu Met Cys Phe Ser Leu Lys  
 485 490 495  
 Leu Arg Asn Arg Lys Leu Pro Arg Phe Leu Glu Glu Val Trp Asp Val  
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 <211> 606  
 <212> PRT  
 <213> Bombyx mori  
  
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 1 5 10 15

Ala Asp Glu Trp Cys Met Ser Val Glu Thr Arg Leu Asp Ser Leu Val  
 20 25 30  
 Arg Glu Lys Ser Glu Val Lys Ala Tyr Val Gly Gly Cys Pro Ser Val  
 35 40 45  
 Ile Thr Asp Ala Gly Ala Tyr Asp Ala Leu Phe Asp Met Arg Arg Arg  
 50 55 60  
 Trp Ser Asn Asn Gly Gly Phe Pro Leu Arg Met Leu Glu Glu Ser Ser  
 65 70 75 80  
 Ser Glu Val Thr Ser Ser Ser Ala Leu Gly Leu Pro Pro Ala Met Val  
 85 90 95  
 Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly Ala Leu Glu Leu  
 100 105 110  
 Trp Ser Tyr Asp Asp Gly Ile Thr Tyr Asn Thr Ala Gln Ser Leu Leu  
 115 120 125  
 Gly Ala Cys Asn Met Gln Gln Gln Gln Leu Gln Pro Gln Gln Pro His  
 130 135 140  
 Pro Ala Pro Pro Thr Leu Pro Thr Met Pro Leu Pro Met Pro Pro Thr  
 145 150 155 160  
 Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly Arg Glu Glu Leu  
 165 170 175  
 Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Ala Asp Ala Asp Ala Arg  
 180 185 190  
 Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu Glu Leu Cys Leu  
 195 200 205  
 Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys  
 210 215 220  
 Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val  
 225 230 235 240  
 Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp Met Tyr Met Arg  
 245 250 255  
 Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met  
 260 265 270  
 Arg Pro Glu Cys Val Ile Gln Glu Pro Ser Lys Asn Lys Asp Arg Gln  
 275 280 285  
 Arg Gln Lys Lys Asp Lys Gly Ile Leu Leu Pro Val Ser Thr Thr Thr  
 290 295 300  
 Val Glu Asp His Met Pro Pro Ile Met Gln Cys Asp Pro Pro Pro Pro  
 305 310 315 320  
 Glu Ala Ala Arg Ile His Glu Val Val Pro Arg Tyr Leu Ser Glu Lys  
 325 330 335  
 Leu Met Glu Gln Asn Arg Gln Lys Asn Ile Pro Pro Leu Ser Ala Asn  
 340 345 350  
 Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr Gln Glu Gly Tyr Glu  
 355 360 365  
 Gln Pro Ser Asp Glu Asp Leu Lys Arg Val Thr Gln Thr Trp Gln Ser  
 370 375 380

Asp Glu Glu Asp Glu Glu Ser Asp Leu Pro Phe Arg Gln Ile Thr Glu  
 385 390 395 400  
 Met Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu  
 405 410 415  
 Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp Gln Ile Thr Leu Leu Lys  
 420 425 430  
 Ala Ser Ser Ser Glu Val Met Met Leu Arg Val Ala Arg Arg Tyr Asp  
 435 440 445  
 Ala Ala Ser Asp Ser Val Leu Phe Ala Asn Asn Lys Ala Tyr Thr Arg  
 450 455 460  
 Asp Asn Tyr Arg Gln Gly Gly Met Ala Tyr Val Ile Glu Asp Leu Leu  
 465 470 475 480  
 His Phe Cys Arg Cys Met Phe Ala Met Gly Met Asp Asn Val His Phe  
 485 490 495  
 Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu  
 500 505 510  
 Gln Pro Ser Leu Val Glu Glu Ile Gln Arg Tyr Tyr Leu Asn Thr Leu  
 515 520 525  
 Arg Ile Tyr Ile Ile Asn Gln Asn Ser Ala Ser Ser Arg Cys Ala Val  
 530 535 540  
 Ile Tyr Gly Arg Ile Leu Ser Val Leu Thr Glu Leu Arg Thr Leu Gly  
 545 550 555 560  
 Thr Gln Asn Ser Asn Met Cys Ile Ser Leu Lys Leu Lys Asn Arg Lys  
 565 570 575  
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 580 585 590  
 Arg His Pro Thr Val Leu Pro Pro Thr Asn Pro Val Val Leu  
 595 600 605  
  
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 <211> 556  
 <212> PRT  
 <213> Manduca sexta  
  
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 20 25 30  
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 35 40 45  
 Gly Leu Glu Leu Trp Ser Tyr Asp Glu Thr Met Thr Asn Tyr Pro Ala  
 50 55 60  
 Gln Ser Leu Leu Gly Ala Cys Asn Ala Pro Gln Gln Gln Gln Gln  
 65 70 75 80  
 Gln Gln Gln Gln Pro Ser Ala Gln Pro Leu Pro Ser Met Pro Leu Pro  
 85 90 95

Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly  
 100 105 110  
 Arg Glu Glu Leu Ser Pro Ala Ser Ser Ile Asn Gly Cys Ser Thr Asp  
 115 120 125  
 Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu  
 130 135 140  
 Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn  
 145 150 155 160  
 Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr  
 165 170 175  
 Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp  
 180 185 190  
 Met Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu  
 195 200 205  
 Ala Val Gly Met Arg Pro Glu Cys Val Val Pro Glu Ser Thr Cys Lys  
 210 215 220  
 Asn Lys Arg Arg Glu Lys Glu Ala Gln Arg Glu Lys Asp Lys Leu Pro  
 225 230 235 240  
 Val Ser Thr Thr Thr Val Asp Asp His Met Pro Ala Ile Met Gln Cys  
 245 250 255  
 Asp Pro Pro Pro Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg  
 260 265 270  
 Phe Leu Thr Glu Lys Leu Met Glu Gln Asn Arg Leu Lys Asn Val Thr  
 275 280 285  
 Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Met Tyr  
 290 295 300  
 Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr  
 305 310 315 320  
 Gln Thr Trp Gln Leu Glu Glu Glu Glu Glu Glu Thr Asp Met Pro  
 325 330 335  
 Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val  
 340 345 350  
 Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp  
 355 360 365  
 Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg  
 370 375 380  
 Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn  
 385 390 395 400  
 Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr  
 405 410 415  
 Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser  
 420 425 430  
 Met Asp Asn Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser  
 435 440 445  
 Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg  
 450 455 460

Tyr Tyr Leu Lys Thr Leu Arg Val Tyr Ile Leu Asn Gln His Ser Ala  
 465 470 475 480

Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr  
 485 490 495

Glu Leu Arg Thr Leu Gly Thr Gln Asn Ser Asn Met Cys Ile Ser Leu  
 500 505 510

Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp  
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Val Ala Glu Val Ser Thr Thr Gln Pro Thr Pro Gly Val Ala Ala Gln  
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Val Thr Pro Ile Val Val Asp Asn Pro Ala Ala Leu  
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<210> 12  
 <211> 675  
 <212> PRT  
 <213> Aedes aegypti

<400> 12

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 1 5 10 15

Met Leu Asp Asp Ser Ser Ser Glu Val Thr Ser Ser Ser Ala Ala Leu  
 20 25 30

Gly Met Thr Met Ser Pro Asn Ser Leu Gly Ser Pro Asn Tyr Asp Glu  
 35 40 45

Leu Glu Leu Trp Ser Ser Tyr Glu Asp Asn Ala Tyr Asn Gly His Ser  
 50 55 60

Val Leu Ser Asn Gly Asn Asn Asn Leu Gly Gly Cys Gly Ala Ala Asn  
 65 70 75 80

Asn Leu Leu Met Asn Gly Ile Val Gly Asn Asn Asn Leu Asn Gly Met  
 85 90 95

Met Asn Met Ala Ser Gln Ala Val Gln Ala Asn Ala Asn Ser Ile Gln  
 100 105 110

His Ile Val Gly Asn Leu Ile Asn Gly Val Asn Pro Asn Gln Thr Leu  
 115 120 125

Ile Pro Pro Leu Pro Ser Ile Ile Gln Asn Thr Leu Met Asn Thr Pro  
 130 135 140

Arg Ser Glu Ser Val Asn Ser Ile Ser Ser Gly Arg Glu Asp Leu Ser  
 145 150 155 160

Pro Ser Ser Ser Leu Asn Gly Tyr Thr Asp Gly Ser Asp Ala Lys Lys  
 165 170 175

Gln Lys Lys Gly Pro Thr Pro Arg Gln Gln Glu Glu Leu Cys Leu Val  
 180 185 190

Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu  
 195 200 205

Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val Tyr  
 210 215 220

Cys Cys Lys Phe Gly His Ala Cys Glu Met Asp Met Tyr Met Arg Arg  
 225 230 235 240  
 Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg  
 245 250 255  
 Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala Ile Lys Arg Lys Glu  
 260 265 270  
 Lys Lys Ala Gln Lys Glu Lys Asp Lys Val Gln Thr Asn Ala Thr Val  
 275 280 285  
 Ser Thr Thr Asn Ser Thr Tyr Arg Ser Glu Ile Leu Pro Ile Leu Met  
 290 295 300  
 Lys Cys Asp Pro Pro Pro His Gln Ala Ile Pro Leu Leu Pro Glu Lys  
 305 310 315 320  
 Leu Leu Gln Glu Asn Arg Leu Arg Asn Ile Pro Leu Leu Thr Ala Asn  
 325 330 335  
 Gln Met Ala Val Ile Tyr Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu  
 340 345 350  
 Gln Pro Ser Glu Glu Asp Leu Lys Arg Ile Met Ile Gly Ser Pro Asn  
 355 360 365  
 Glu Glu Glu Asp Gln His Asp Val His Phe Arg His Ile Thr Glu Ile  
 370 375 380  
 Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu Pro  
 385 390 395 400  
 Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys Ala  
 405 410 415  
 Cys Ser Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp Ala  
 420 425 430  
 Ala Thr Asp Ser Ile Leu Phe Ala Asn Asn Arg Ser Tyr Thr Arg Asp  
 435 440 445  
 Ser Tyr Arg Met Ala Gly Met Ala Asp Thr Ile Glu Asp Leu Leu His  
 450 455 460  
 Phe Cys Arg Gln Met Phe Ser Leu Thr Val Asp Asn Val Glu Tyr Ala  
 465 470 475 480  
 Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu Gln  
 485 490 495  
 Ala Glu Leu Val Glu His Ile Gln Ser Tyr Tyr Ile Asp Thr Leu Arg  
 500 505 510  
 Ile Tyr Ile Leu Asn Arg His Ala Gly Asp Pro Lys Cys Ser Val Ile  
 515 520 525  
 Phe Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn  
 530 535 540  
 Gln Asn Ser Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys Leu  
 545 550 555 560  
 Pro Arg Phe Leu Glu Glu Ile Trp Asp Val Gln Asp Ile Pro Pro Ser  
 565 570 575  
 Met Gln Ala Gln Met His Ser His Gly Thr Gln Ser Ser Ser Ser Ser  
 580 585 590

Ser Ser Ser Ser Ser Ser Ser Ser Asn Gly Ser Ser Asn Gly Asn Ser  
 595 600 605  
 Ser Ser Asn Ser Asn Ser Ser Gln His Gly Pro His Pro His Pro His  
 610 615 620  
 Gly Gln Gln Leu Thr Pro Asn Gln Gln Gln His Gln Gln Gln His Ser  
 625 630 635 640  
 Gln Leu Gln Gln Val His Ala Asn Gly Ser Gly Ser Gly Gly Gly Ser  
 645 650 655  
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 Asp Gln Val  
 675  
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 <211> 319  
 <212> PRT  
 <213> *Heliothis virescens*  
 <400> 13  
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 1 5 10 15  
 Glu Lys Lys Ala Gln Arg Glu Lys Asp Lys Leu Pro Val Ser Thr Thr  
 20 25 30  
 Thr Val Asp Asp His Met Pro Pro Ile Met Gln Cys Asp Pro Pro Pro  
 35 40 45  
 Pro Glu Ala Ala Arg Ile Leu Glu Cys Val Gln His Glu Val Val Pro  
 50 55 60  
 Arg Phe Leu Asn Glu Lys Leu Met Glu Gln Asn Arg Leu Lys Asn Val  
 65 70 75 80  
 Pro Pro Leu Thr Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp  
 85 90 95  
 Tyr Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val  
 100 105 110  
 Thr Gln Ser Asp Glu Asp Asp Glu Asp Ser Asp Met Pro Phe Arg Gln  
 115 120 125  
 Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala  
 130 135 140  
 Lys Gly Leu Pro Gly Phe Ala Lys Ile Ser Gln Ser Asp Gln Ile Thr  
 145 150 155 160  
 Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Val Ala Arg  
 165 170 175  
 Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn Asn Gln Ala  
 180 185 190  
 Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ala Tyr Val Ile Glu  
 195 200 205  
 Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Met Met Asp Asn  
 210 215 220

Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg Pro  
 225 230 235 240  
 Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg Tyr Tyr Leu  
 245 250 255  
 Asn Thr Leu Arg Val Tyr Ile Leu Asn Gln Asn Ser Ala Ser Pro Arg  
 260 265 270  
 Gly Ala Val Ile Phe Gly Glu Ile Leu Gly Ile Leu Thr Glu Ile Arg  
 275 280 285  
 Thr Leu Gly Met Gln Asn Ser Asn Met Cys Ile Ser Leu Lys Leu Lys  
 290 295 300  
 Lys Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Asp Trp Asp Val  
 305 310 315

<210> 14  
 <211> 8  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Conserved motif within DNA binding domain of RAR and THR  
 receptors

<400> 14

Cys Glu Gly Cys Lys Gly Phe Phe  
 1 5

<210> 15  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Degenerate sense oligonucleotide

<220>  
 <221> misc\_feature  
 <222> (1)..(23)  
 <223> y=c or t

<220>  
 <221> misc\_feature  
 <222> (1)..(23)  
 <223> r=g or a

<220>  
 <221> misc\_feature  
 <222> (1)..(23)  
 <223> n=inosine

<400> 15  
 tgygarggnt gyaargantt ytt

23

<210> 16  
 <211> 8  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Peptide sequence corresponding to conserved motif used for  
 degenerate antisense oligonucleotide

<220>

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<221> MISC_FEATURE
<222> (3)..(3)
<223> X=E or S

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X=L or R

<400> 16

Cys Gln Xaa Cys Arg Xaa Lys Lys
1 5

<210> 17
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Degenerate oligo ZnFA3'

<220>
<221> misc_feature
<222> (1)..(23)
<223> r=g or a

<220>
<221> misc_feature
<222> (1)..(23)
<223> y=c or t

<220>
<221> misc_feature
<222> (1)..(23)
<223> n=inosine

<400> 17
ttyttnagnc grcaytcytg rca

<210> 18
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Degenerate oligo ZnFB3'

<220>
<221> misc_feature
<222> (1)..(23)
<223> r=g or a

<220>
<221> misc_feature
<222> (1)..(23)
<223> y=c or t

<220>
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<222> (1)..(23)
<223> n=inosine

<400> 18
ttyttnaanc grcaytcytg rca

<210> 19
<211> 23

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23

23

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<212> DNA
<213> Artificial

<220>
<223> Degenerate oligo ZnFC3'

<220>
<221> misc_feature
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<223> r=g or a

<220>
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<222> (1)..(23)
<223> y=c or t

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<221> misc_feature
<222> (1)..(23)
<223> n=inosine

<400> 19
ttyttnagnc trcaytcytcg rca 23

<210> 20
<211> 23
<212> DNA
<213> Artificial

<220>
<223> Degenerate oligo ZnFD3'

<220>
<221> misc_feature
<222> (1)..(23)
<223> r=g or a

<220>
<221> misc_feature
<222> (1)..(23)
<223> y=c or t

<220>
<221> misc_feature
<222> (1)..(23)
<223> n=inosine

<400> 20
ttyttnaanc trcaytcytcg rca 23

<210> 21
<211> 39
<212> DNA
<213> Artificial

<220>
<223> PCR sense oligonucleotide used to isolate the full 5' end
sequence of H. virescens gene

<400> 21
aattaagctt ccaccatgcc gttaccaatg ccaccgaca 39

<210> 22
<211> 20
<212> DNA
<213> Artificial

<220>

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<223> Antisense primer used to isolate correct 5' end of *H. virescens* gene

<400> 22  
cttcaaccga cactcctgac 20

<210> 23  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<223> Sense primer used to isolate correct 5' end of *H. virescens* gene

<400> 23  
cagctccagg ccgccgatct cg 22

<210> 24  
<211> 48  
<212> DNA  
<213> Artificial

<220>  
<223> Anchor primer used to isolate correct 5' end of *H. virescens* gene

<220>  
<221> misc\_feature  
<222> (1)..(48)  
<223> n=inosine

<400> 24  
cuacuacuac uaggccacgc gtcgactagt acgggnnggg nngggngg 48

<210> 25  
<211> 32  
<212> DNA  
<213> Artificial

<220>  
<223> Universal amplification primer used to isolate correct 5' end of *H. virescens* gene

<400> 25  
caucaucauc auggccacgc gtcgactagt ac 32

<210> 26  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Primer used to isolate correct 5' end of *H. virescens* gene

<400> 26  
acgtcacctc agacgagctc tccattc 27

<210> 27  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<223> Primer used to confirm correct 5' end of *H. virescens* gene

<400> 27  
cgctggtata acaacggacc attc 24

<210> 28

<211> 48  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Primer used to incorporate HindIII site, Kozak consensus sequence, and Met-Arg-Arg into third effector construct  
  
 <400> 28  
 attaagcttg ccgccatgcg ccgacgctgg tataacaacg gaccattc 48  
  
 <210> 29  
 <211> 39  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Sense oligo used to introduce HindIII site and Kozak consensus sequence into fourth effector construct  
  
 <400> 29  
 attaagcttg ccgccatgct cctcggcgct cgtggatac 39  
  
 <210> 30  
 <211> 137  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligo that is complementary to SEQ ID NO: 31, which when annealed encode tandem repeats of the ecdysone response element flanked by SpeI and ClaI sites  
  
 <400> 30  
 ctagtagaca aggggttcaat gcacttgctc aataagctta gacaagggtt caatgcactt 60  
 gtccaatgaa ttcagacaag ggttcaatgc acttgctcaa tctgcagaga caagggttca 120  
 atgcacttgt ccaatat 137  
  
 <210> 31  
 <211> 135  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> Oligo that is complementary to SEQ ID NO: 30, which when annealed encode tandem repeats of the ecdysone response element flanked by SpeI and ClaI sites  
  
 <400> 31  
 cgatattgga caagtgcatt gaacccttgt ctctgcagat tggacaagtg cattgaaccc 60  
 ttgtctgaat tcattggaca agtgcatgga acccttgtct aagcttattg gacaagtgca 120  
 ttgaaccctt gtcta 135  
  
 <210> 32  
 <211> 38  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> PCR primer used to incorporate an EcoRI site and a Kozak consensus sequence into an expression construct  
  
 <400> 32  
 attgaattcc accatggact ccaaagaatc attaactc 38

<210> 33  
 <211> 42  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> 3' primer used to incorporate an XhoI site in frame with the  
 reading frame at amino acid 500 of the human glucocorticoid  
 receptor  
  
 <400> 33  
 gagactcctg tagtggcctc gagcattcct tttatttttt tc 42  
  
 <210> 34  
 <211> 31  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> 5' primer incorporating an XhoI site at amino acid 500 of the  
 human glucocorticoid receptor  
  
 <400> 34  
 attctcgaga ttcagcaggc cactacagga g 31  
  
 <210> 35  
 <211> 32  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> 3' primer used to incorporate an EcoRI site 400 bp downstream of  
 the human glucocorticoid receptor ORF  
  
 <400> 35  
 attgaattca atgctatcgt aactatacag gg 32  
  
 <210> 36  
 <211> 35  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> 5' oligo containing a SalI site at the beginning of the hinge  
 region of the Drosophila ecdysone receptor cDNA  
  
 <400> 36  
 attgtcgaca acggccggaa tggctcgtcc cggag 35  
  
 <210> 37  
 <211> 48  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> 3' oligo used to incorporate a BamHI site adjacent to the stop  
 codon of the Drosophila ecdysone receptor cDNA  
  
 <400> 37  
 tcgggctttg ttaggatcct aagccgtggt cgaatgctcc gacttaac 48  
  
 <210> 38  
 <211> 35  
 <212> DNA  
 <213> Artificial  
  
 <220>

<223> Oligo used to incorporate a SalI site at the DNAbinding/hinge domain junction of hte Heliothis ecdysone receptor cDNA

<400> 38  
attgtcgaca aaggcccgag tgcgtggtgc cggag 35

<210> 39  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<223> Primer used to achieve PCR-mediated mutagenesis adding a SalI site downstream of the DNA binding/hinge domain junction

<400> 39  
tcacattgca tgatgggagg catg 24

<210> 40  
<211> 82  
<212> DNA  
<213> Artificial

<220>  
<223> Oligo that anneals to SEQ ID NO: 41 to produce a double-stranded DNA encoding six copies of hte glucocorticoid response element flanked by HindIII and SalI sites

<400> 40  
agcttcgact gtacaggatg ttctagctac tcgagtagct agaacatcct gtacagtcga 60  
gtagctagaa catcctgtac ag 82

<210> 41  
<211> 82  
<212> DNA  
<213> Artificial

<220>  
<223> Oligo that anneals to SEQ ID NO: 40 to produce a double-stranded DNA encoding six copies of hte glucocorticoid response element flanked by HindIII and SalI sites

<400> 41  
tcgactgtac aggatgttct agctactcga ctgtacagga tgttctagct actcgagtcg 60  
ctagaacatc ctgtacagtc ga 82

<210> 42  
<211> 78  
<212> DNA  
<213> Artificial

<220>  
<223> Oligo that anneals to SEQ ID NO: 43 to produce a double-stranded DNA encoding six copies of hte glucocorticoid response element flanked by SalI and BanHI sites

<400> 42  
tcgactagct agaacatcct gtacagtcga gtagctagaa catcctgtac agtcgagtag 60  
ctagaacatc ctgtacag 78

<210> 43  
<211> 78  
<212> DNA  
<213> Artificial

<220>  
 <223> Oligo that anneals to SEQ ID NO: 42 to produce a double-stranded DNA encoding six copies of the glucocorticoid response element flanked by SalI and BanHI sites

<400> 43  
 gatcctgtac aggatgttct agctactcga ctgtacagga tgttctagct actcgactgt 60  
 acaggatggt ctagctag 78

<210> 44  
 <211> 104  
 <212> DNA  
 <213> Artificial

<220>  
 <223> 5' oligo used with SEQ ID NO: 45 to incorporate 4 copies of the glucocorticoid response element flanked by SpeI and AflII sites into pSWBGAL

<400> 44  
 ctagtgttac aggatgttct agctactcga gtagctagaa catcctgtac agtcgagtag 60  
 ctagaacatc ctgtacagtc gagtagctag aacatcctgt acac 104

<210> 45  
 <211> 104  
 <212> DNA  
 <213> Artificial

<220>  
 <223> 3' oligo used with SEQ ID NO: 44 to incorporate 4 copies of the glucocorticoid response element flanked by SpeI and AflII sites into pSWBGAL

<400> 45  
 ttaagtgtac aggatgttct agctactcga ctgtacagga tgttctagct actcgactgt 60  
 acaggatggt ctagctactc gagtagctag aacatcctgt acaa 104

<210> 46  
 <211> 15  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Oligo that in conjunction with SEQ ID NO: 47 creates an ApaI/NotI linker

<400> 46  
 cattggatcc ttagc 15

<210> 47  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Oligo that in conjunction with SEQ ID NO: 46 creates an ApaI/NotI linker

<400> 47  
 ggccgctaag gatccaatgg gcc 23

<210> 48  
 <211> 32  
 <212> DNA  
 <213> Artificial

<220>  
 <223> 5' oligo used to introduce an NcoI site into amino acid 259 of the *Heliothis ecdysone* receptor ORF

<400> 48 32  
 aattccatgg tacgacgaca gtagacgatc ac

<210> 49  
 <211> 29  
 <212> DNA  
 <213> Artificial

<220>  
 <223> 3' oligo used to introduce an XbaI site flanking amino acid 571 of the *Heliothis ecdysone* receptor ORF

<400> 49 29  
 ctgaggtcta gagacggtgg cgggcggcc

<210> 50  
 <211> 31  
 <212> DNA  
 <213> Artificial

<220>  
 <223> 5' oligo used to introduce Kozak consensus sequences, a methionine start codon, and an coding sequence up to amino acid 152 of the glucocorticoid receptor, with an upstream EcoRI site

<400> 50 31  
 atatgaattc caccatggac tccaaagaat c

<210> 51  
 <211> 36  
 <212> DNA  
 <213> Artificial

<220>  
 <223> 3' oligo used to introduce Kozak consensus sequences, a methionine start codon, and an coding sequence up to amino acid 152 of the glucocorticoid receptor, and a downstream NheI site

<400> 51 36  
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<210> 52  
 <211> 33  
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 <213> Artificial

<220>  
 <223> 5' primer that incorporates an NheI site into the codon for amino acid 406 of the glucocorticoid receptor

<400> 52 33  
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<210> 53  
 <211> 30  
 <212> DNA  
 <213> Artificial

<220>  
 <223> 3' oligo that incorporates an XhoI site at amino acid 500 of the glucocorticoid receptor

<400> 53

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<210> 54  
 <211> 30  
 <212> DNA  
 <213> Artificial

<220>  
 <223> 5' oligo used to amplify amino acids 411-490 of the herpes simplex VP16 protein, incorporating flanking SpeI sites

<400> 54  
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<210> 55  
 <211> 31  
 <212> DNA  
 <213> Artificial

<220>  
 <223> 3' oligo used to amplify amino acids 411-490 of the herpes simplex VP16 protein, incorporating flanking SpeI sites

<400> 55  
 aattactagt cccaccgtac tcgtcaattc c 31

<210> 56  
 <211> 32  
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 <223> w=t or a

<220>  
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 <223> k=g or t

<400> 56  
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<210> 57  
 <211> 32  
 <212> DNA  
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<220>  
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 <223> n=inosine

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<223> w=t or a

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<223> s=g or c

<400> 57
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<210> 58
<211> 33
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domains from other lepidopteran species

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<223> w=t or a

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<400> 58
ttactcgagn acgwcccana tctctycnag gaa 33

<210> 59
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<213> Artificial

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domains from other lepidopteran species

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<223> y=c or t

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